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Om protein - protein search, using sw model

Run on: August 28, 2002, 17:39:04 ; Search time 79.38 Seconds (without alignments)

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 747981 seqs, 24205750 residues

Total number of hits satisfying chosen parameters: 747981

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

1: Pending_Patents_AA_New;*

2: /cgn2_6/potodata/1/paa/US06_NEW_COMBO.pep;*

3: /cgn2_6/potodata/1/paa/US07_NEW_COMBO.pep;*

4: /cgn2_6/potodata/1/paa/US08_NEW_COMBO.pep;*

5: /cgn2_6/potodata/1/paa/US09_NEW_COMBO.pep;*

6: /cgn2_6/potodata/1/paa/US10_NEW_COMBO.pep;*

7: /cgn2_6/potodata/1/paa/US60_NEW_COMBO.pep;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1284	100.0	249	5 US-09-502-984B-37
2	1098	85.5	211	5 US-09-502-984B-6
3	1080	84.1	211	5 US-09-502-984B-5
4	1078	84.0	211	5 US-09-502-984B-4
5	1075	83.7	211	5 US-09-502-984B-9
6	1073	83.6	211	5 US-09-502-984B-13
7	1073	83.6	211	5 US-09-502-984B-14
8	1073	83.6	211	5 US-09-502-984B-15
9	1070	83.3	211	5 US-09-502-984B-7
10	1070	83.3	211	5 US-09-502-984B-17
11	1066	83.0	211	5 US-09-502-984B-16
12	1064	82.9	211	5 US-09-502-984B-11
13	1061	82.6	211	5 US-09-502-984B-12
14	1060	82.6	211	5 US-09-502-984B-2
15	1060	82.6	211	5 US-09-502-984B-10
16	1060	82.6	211	5 US-09-502-984B-1
17	1060	82.6	213	5 US-09-791-537-67299
18	1060	82.6	215	5 US-09-791-537-105911
19	1050	82.6	225	5 US-09-502-984B-1
20	1060	82.6	508	5 US-09-791-537-99806
21	1059.5	82.5	212	5 US-09-502-984B-3
22	1053	82.0	211	5 US-09-502-984B-8
23	1048	81.6	211	5 US-09-502-984B-18
24	1043	81.2	227	5 US-09-791-537-68105
25	1043	81.2	228	5 US-09-791-537-38134
26	1039	80.9	211	5 US-09-502-984B-19

ALIGNMENTS

RESULT 1
US-09-502-984B-37
; Sequence 37, Application US/09502984B
; GENERAL INFORMATION:
; APPLICANT: Luo, Peizhi
; TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES FOR DRUG DISCOVERY
; FILE REFERENCE: A-68126-1/RIT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/502, 984B
; CURRENT FILING DATE: 2000-02-11
; PRIORITY APPLICATION NUMBER: 60/120, 009
; PRIORITY FILING DATE: 1999-02-11
; PRIORITY APPLICATION NUMBER: 60/131, 674
; PRIORITY FILING DATE: 1999-04-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-09-502-984B-37

Query Match Score 100.0%; Score 1284; DB 5; Length 249; Best Local Similarity 100.0%; Pred. No. 1.4e-108; Indels 0; Gaps 0; Gaps 0; Mismatches 0; Sequence 1, Appli

QY 1 KFESKAALLAARGPPEELLCFTERLELDIVCFEEAASAGVGPONFSISFOLEDEPKICRL 60
Db 1 KFESKAALLAARGPPEELLCFTERLELDIVCFEEAASAGVGPONFSISFOLEDEPKICRL 60

QY 61 HOAPARTGAIREFWCSLPTADTSSFPVPLRITAASCPAPRFHRVHINENVILDAPGVVA 120
Db 61 HOAPARTGAIREFWCSLPTADTSSFPVPLRITAASCPAPRFHRVHINENVILDAPGVVA 120

QY 121 RLADESHWVIRLWLPPETPMTHIRELDISAGNGGSVQRVELLEGRTCEVLSNUR 180
Db 121 RLADESHWVIRLWLPPETPMTHIRELDISAGNGGSVQRVELLEGRTCEVLSNUR 180

QY 181 TRITAVARMAEPSPGGFWSAWSEPVSLTGGGSRMKEIQLVKELRKNERLEEVE 240
Db 181 TRITAVARMAEPSPGGFWSAWSEPVSLTGGGSRMKEIQLVKELRKNERLEEVE 240

QY 241 RLQOLVGER 249
Db 241 RLQOLVGER 249

RESULT 2
US-09-502-984B-6
; Sequence 6, Application US/09502984B
; GENERAL INFORMATION:
; APPLICANT: LUO, Peizhi
; TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES FOR DRUG DISCOVERY
; FILE REFERENCE: A-68126-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/502, 984B
; CURRENT FILING DATE: 2000-02-11
; PRIORITY NUMBER: 60/120, 009
; PRIORITY FILING DATE: 1999-02-11
; PRIORITY APPLICATION NUMBER: 60/131, 674
; PRIORITY FILING DATE: 1999-04-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; US-09-502-984B-6

Query Match 85.5%; Score 1098; DB 5; Length 211;
Best Local Similarity 100.0%; Pred. No. 8 7e-92; Mismatches 0; Indels 0; Gaps 0;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFESKAALLAARGPPEELCFTTERLEDVCFEEAASAGVGCGNFSFSQLEDEPWKLICRL 60
Db 1 KFESKAALLAARGPPEELCFTTERLEDVCFEEAASAGVGCGNFSFSQLEDEPWKLICRL 60

QY 61 HQAPTAGAIRFWCSLPTADTSFVPLRLTAASGAPRHRVHINEVVLIDAPVGLVA 120
Db 61 HQAPTAGAVRFWCSLPTADTSFVPLRLTAASGAPRHRVHINEVVLIDAPVGLVA 120

QY 121 RLADESGHVVIRWLPPETPMASHIREVLDISAGNGAGSVQRVELLEGRTCEVLSNLRGR 180
Db 121 RLADESGHVVIRWLPPETPMASHIREVLDISAGNGAGSVQRVELLEGRTCEVLSNLRGR 180

QY 181 TRITIAVRARMAPSFEGFWSAWSEPVSLT 211
Db 181 TRITIAVRARMAPSFEGFWSAWSEPVSLT 211

RESULT 4
US-09-502-984B-4
; Sequence 4, Application US/09502984B
; GENERAL INFORMATION:
; APPLICANT: LUO, Peizhi
; TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES FOR DRUG DISCOVERY
; FILE REFERENCE: A-68126-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/502, 984B
; PRIORITY NUMBER: 60/120, 009
; PRIORITY FILING DATE: 1999-02-11
; PRIORITY APPLICATION NUMBER: 60/131, 674
; PRIORITY FILING DATE: 1999-04-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; US-09-502-984B-4

Query Match 84.0%; Score 1078; DB 5; Length 211;
Best Local Similarity 96.7%; Pred. No. 5 7e-92; Mismatches 5; Indels 0; Gaps 0;
Matches 204; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 KFESKAALLAARGPPEELCFTTERLEDVCFEEAASAGVGCGNFSFSQLEDEPWKLICRL 60
Db 1 KFESKAALLAARGPPEELCFTTERLEDVCFEEAASAGVGCGNFSFSQLEDEPWKLICRL 60

QY 61 HQAPTAGAIRFWCSLPTADTSFVPLRLTAASGAPRHRVHINEVVLIDAPVGLVA 120
Db 61 HQAPTAGAIRFWCSLPTADTSFVPLRLTAASGAPRHRVHINEVVLIDAPVGLVA 120

QY 121 RLADESGHVVIRWLPPETPMASHIREVLDISAGNGAGSVQRVELLEGRTCEVLSNLRGR 180
Db 121 RLADESGHVVIRWLPPETPMASHIREVLDISAGNGAGSVQRVELLEGRTCEVLSNLRGR 180

QY 181 TRITIAVRARMAPSFEGFWSAWSEPVSLT 211
Db 181 TRITIAVRARMAPSFEGFWSAWSEPVSLT 211

RESULT 5
US-09-502-984B-9
; Sequence 9, Application US/09502984B
; GENERAL INFORMATION:
; APPLICANT: LUO, Peizhi
; TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES FOR DRUG DISCOVERY
; FILE REFERENCE: A-68126-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/502, 984B
; CURRENT FILING DATE: 2000-02-11
; PRIORITY NUMBER: 60/120, 009
; PRIORITY FILING DATE: 1999-02-11

Query Match 84.1%; Score 1080; DB 5; Length 211;
Best Local Similarity 97.2%; Pred. No. 3 8e-90; Mismatches 6; Indels 0; Gaps 0;
Matches 205; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

PRIOR APPLICATION NUMBER: 60/131, 674
 PRIOR FILING DATE: 1999-04-29
 NUMBER OF SEQ ID NOS: 37
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 9
 LENGTH: 211
 TYPE: PRT
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC

US-09-502-984B-9

Query Match 83.7%; Score 1075; DB 5; Length 211;
 Best Local Similarity 96.2%; Pred. No. 1, 1e-89; Mismatches 203; Conservative 6; MisMatches 2; Indels 0; Gaps 0;

QY 1 KFESKAALLAARGPPEELCFTTERLEDIVCFEEAASAGVGPGNFNSFSFOLDEDEPWKLTRL 60
 1 KFESKAALLAARGPPEELCFTTERLEDIVCFEEAASAGVGPGNFNSFSFOLDEDEPWKLTRL 60

Db 61 HOAPTARGAIRFWCSLPTADISSFPVPLRLTAASGAPRFHRVHINEVWILDAPVGLVA 120
 61 HOAPTARGAIRFWCSLPTADISSFPVPLRLTAASGAPRFHRVHINEVWILDAPVGLVA 120

Db 61 TRYFAVARMARMAEPSFGFWSAWSEPVSLT 211
 61 TRYFAVARMARMAEPSFGFWSAWSEPVSLT 211

QY 121 RLADESCHWVIRWLPPPETPMTHIRELDISAGNGAGSVORVELLEGRCVLSNLRGR 180
 121 RLADESCHWVIRWLPPPETPMTHIRELDISAGNGAGSVORVELLEGRCVLSNLRGR 180

QY 181 TRITIAVARMARMAEPSFGFWSAWSEPVSLT 211
 181 TRYFAVARMARMAEPSFGFWSAWSEPVSLT 211

Db 181 TRYFAVARMARMAEPSFGFWSAWSEPVSLT 211
 181 TRYFAVARMARMAEPSFGFWSAWSEPVSLT 211

RESULT 6

US-09-502-984B-13

; Sequence 13, Application US/09502984B
 ; GENERAL INFORMATION:
 ; APPLICANT: Luo, Peizhi
 ; TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES FOR DRUG DISCOVERY
 ; FILE REFERENCE: A-68126-1/RET/RMS/RMK
 ; CURRENT APPLICATION NUMBER: US/09/502, 984B
 ; CURRENT APPLICATION NUMBER: US/09/502, 984B
 ; CURRENT FILING DATE: 2000-02-11
 ; PRIOR APPLICATION NUMBER: 60/120, 009
 ; PRIOR FILING DATE: 1999-02-11
 ; PRIOR APPLICATION NUMBER: 60/131, 674
 ; PRIOR FILING DATE: 1999-04-29
 ; NUMBER OF SEQ ID NOS: 37
 ; SEQ ID NO 13
 ; LENGTH: 211
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE: PRT
 ; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC

US-09-502-984B-14

Query Match 83.6%; Score 1073; DB 5; Length 211;
 Best Local Similarity 96.2%; Pred. No. 1, 6e-89; Mismatches 203; Conservative 6; MisMatches 2; Indels 0; Gaps 0;

QY 1 KFESKAALLAARGPPEELCFTTERLEDIVCFEEAASAGVGPGNFNSFSFOLDEDEPWKLTRL 60
 Db 1 KFESKAALLAARGPPEELCFTTERLEDIVCFEEAASAGVGPGNFNSFSFOLDEDEPWKLTRL 60

QY 61 HOAPTARGAIRFWCSLPTADISSFPVPLRLTAASGAPRFHRVHINEVWILDAPVGLVA 120
 61 HOAPTARGAIRFWCSLPTADISSFPVPLRLTAASGAPRFHRVHINEVWILDAPVGLVA 120

Db 121 RLADESCHWVIRWLPPPETPMTHIRELDISAGNGAGSVORVELLEGRCVLSNLRGR 180
 121 RLADESCHWVIRWLPPPETPMTHIRELDISAGNGAGSVORVELLEGRCVLSNLRGR 180

QY 181 TRITIAVARMARMAEPSFGFWSAWSEPVSLT 211
 181 TRYFAVARMARMAEPSFGFWSAWSEPVSLT 211

Db 181 TRYFAVARMARMAEPSFGFWSAWSEPVSLT 211
 181 TRYFAVARMARMAEPSFGFWSAWSEPVSLT 211

RESULT 8

US-09-502-984B-15

; Sequence 15, Application US/09502984B
 ; GENERAL INFORMATION:
 ; APPLICANT: Luo, Peizhi
 ; TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES FOR DRUG DISCOVERY
 ; FILE REFERENCE: A-68126-1/RET/RMS/RMK
 ; CURRENT APPLICATION NUMBER: US/09/502, 984B
 ; CURRENT APPLICATION NUMBER: US/09/502, 984B
 ; CURRENT FILING DATE: 2000-02-11
 ; PRIOR APPLICATION NUMBER: 60/120, 009
 ; PRIOR FILING DATE: 1999-02-11
 ; PRIOR APPLICATION NUMBER: 60/131, 674
 ; PRIOR FILING DATE: 1999-04-29
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 15
 ; LENGTH: 211
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE: PRT
 ; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC

US-09-502-984B-15

Query Match 83.6%; Score 1073; DB 5; Length 211;
 Best Local Similarity 96.2%; Pred. No. 1 6e-89; Mismatches 6; Indels 0; Gaps 0;
 Matches 203; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KFESKAALLAARGPPEELCFTERLEDIVCFEEAASAGVPGNFSFSFQLEDEPWKLTRL 60
 Db 1 KFESKAALLAARGPPEELCFTERLEDIVCFEEAASAGVPGNFSFSFQLEDEPWKLTRL 60

Qy 61 HOAPTAGRAFWCSLPTADSSFVPLRITAASGAPRFHRVHINEVWILDAPVGLVA 120
 Db 61 HOAPTAGRAFWCSLPTADSSFVPLRITAASGAPRFHRVHINEVWILDAPVGLVA 120

Qy 181 TRITIAYARMARAEPSFGFWSAWSEPVSLT 211
 Db 181 TRYFAVRARMAEPSPFGFWSAWSEPVSLT 211

Query Match 83.5%; Score 1073; DB 5; Length 211;
 Best Local Similarity 96.2%; Pred. No. 1 6e-89; Mismatches 6; Indels 0; Gaps 0;
 Matches 203; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KFESKAALLAARGPPEELCFTERLEDIVCFEEAASAGVPGNFSFSFQLEDEPWKLTRL 60
 Db 1 KFESKAALLAARGPPEELCFTERLEDIVCFEEAASAGVPGNFSFSFQLEDEPWKLTRL 60

Qy 61 HOAPTAGRAFWCSLPTADSSFVPLRITAASGAPRFHRVHINEVWILDAPVGLVA 120
 Db 61 HOAPTAGRAFWCSLPTADSSFVPLRITAASGAPRFHRVHINEVWILDAPVGLVA 120

Qy 121 RLADESCHVIRWLPPETPMTHIRELDISAGNGAGSVORVEILEGRTECVLSNLGR 180
 Db 121 RLADESCHVIRWLPPETPMTHIRELDISAGNGAGSVORVEILEGRTECVLSNLGR 180

Qy 121 RLADESCHVIRWLPPETPMTHIRELDISAGNGAGSVORVEILEGRTECVLSNLGR 180
 Db 121 RLADESCHVIRWLPPETPMTHIRELDISAGNGAGSVORVEILEGRTECVLSNLGR 180

Qy 181 TRITIAYARMARAEPSFGFWSAWSEPVSLT 211
 Db 181 TRYFAVRARMAEPSPFGFWSAWSEPVSLT 211

Query Match 83.3%; Score 1070; DB 5; Length 211;
 Best Local Similarity 94.3%; Pred. No. 3.1e-89; Mismatches 0; Indels 0; Gaps 0;
 Matches 199; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFESKAALLAARGPPEELCFTERLEDIVCFEEAASAGVPGNFSFSFQLEDEPWKLTRL 60
 Db 1 KFESKAALLAARGPPEELCFTERLEDIVCFEEAASAGVPGNFSFSFQLEDEPWKLTRL 60

Qy 61 HOAPTAGRAFWCSLPTADSSFVPLRITAASGAPRFHRVHINEVWILDAPVGLVA 120
 Db 61 HOAPTAGRAFWCSLPTADSSFVPLRITAASGAPRFHRVHINEVWILDAPVGLVA 120

Qy 121 RLADESCHVIRWLPPETPMTHIRELDISAGNGAGSVORVEILEGRTECVLSNLGR 180
 Db 121 RLADESCHVIRWLPPETPMTHIRELDISAGNGAGSVORVEILEGRTECVLSNLGR 180

Qy 181 TRITIAYARMARAEPSFGFWSAWSEPVSLT 211
 Db 181 TRITIAYARMARAEPSFGFWSAWSEPVSLT 211

Query Match 83.3%; Score 1070; DB 5; Length 211;
 Best Local Similarity 94.3%; Pred. No. 3.1e-89; Mismatches 0; Indels 0; Gaps 0;
 Matches 199; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFESKAALLAARGPPEELCFTERLEDIVCFEEAASAGVPGNFSFSFQLEDEPWKLTRL 60
 Db 1 KFESKAALLAARGPPEELCFTERLEDIVCFEEAASAGVPGNFSFSFQLEDEPWKLTRL 60

Qy 61 HOAPTAGRAFWCSLPTADSSFVPLRITAASGAPRFHRVHINEVWILDAPVGLVA 120
 Db 61 HOAPTAGRAFWCSLPTADSSFVPLRITAASGAPRFHRVHINEVWILDAPVGLVA 120

Qy 121 RLADESCHVIRWLPPETPMTHIRELDISAGNGAGSVORVEILEGRTECVLSNLGR 180
 Db 121 RLADESCHVIRWLPPETPMTHIRELDISAGNGAGSVORVEILEGRTECVLSNLGR 180

Qy 181 TRITIAYARMARAEPSFGFWSAWSEPVSLT 211
 Db 181 TRYFAVRARMAEPSPFGFWSAWSEPVSLT 211

Query Match 83.3%; Score 1070; DB 5; Length 211;
 Best Local Similarity 94.3%; Pred. No. 3.1e-89; Mismatches 0; Indels 0; Gaps 0;
 Matches 199; Conservative 12; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFESKAALLAARGPPEELCFTERLEDIVCFEEAASAGVPGNFSFSFQLEDEPWKLTRL 60
 Db 1 KFESKAALLAARGPPEELCFTERLEDIVCFEEAASAGVPGNFSFSFQLEDEPWKLTRL 60

Qy 61 HOAPTAGRAFWCSLPTADSSFVPLRITAASGAPRFHRVHINEVWILDAPVGLVA 120
 Db 61 HOAPTAGRAFWCSLPTADSSFVPLRITAASGAPRFHRVHINEVWILDAPVGLVA 120

Qy 121 RLADESCHVIRWLPPETPMTHIRELDISAGNGAGSVORVEILEGRTECVLSNLGR 180
 Db 121 RLADESCHVIRWLPPETPMTHIRELDISAGNGAGSVORVEILEGRTECVLSNLGR 180

Qy 181 TRITIAYARMARAEPSFGFWSAWSEPVSLT 211
 Db 181 TRYFAVRARMAEPSPFGFWSAWSEPVSLT 211

Query Match 83.0%; Score 1066; DB 5; Length 211;
 Best Local Similarity 93.8%; Pred. No. 7e-89; Mismatches 1; Indels 0; Gaps 0;
 Matches 198; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KFESKAALLAARGPPEELCFTERLEDIVCFEEAASAGVPGNFSFSFQLEDEPWKLTRL 60
 Db 1 KFESKAALLAARGPPEELCFTERLEDIVCFEEAASAGVPGNFSFSFQLEDEPWKLTRL 60

Qy 61 HOAPTAGRAFWCSLPTADSSFVPLRITAASGAPRFHRVHINEVWILDAPVGLVA 120
 Db 61 HOAPTAGRAFWCSLPTADSSFVPLRITAASGAPRFHRVHINEVWILDAPVGLVA 120

Db 61 HQAPTAGVRFWCSLPTADTSFVPLRVTASGAPRHVTHINNEVLLDAPVGLV 120
 Qy 121 RLADSGHVVIRWLPPETPTMHSIRFIELDISAGNGAGSVORVELLEGRTCEVLNSLRGR 180
 Db 121 RLADSGHVVIRWLPPETPTMHSIRFIELDISAGNGAGSVORVELLEGRTCEVLNSLRGR 180

Qy 181 TRITAVRVARMAEPSFGGFWSAWSEPVSLT 211
 Db 181 TRITAVRVARMAEPSFGGFWSAWSEPVSLT 211

RESULT 12
 US-09-502-984B-11
 ; Sequence 11, Application US/09502984B
 ; GENERAL INFORMATION:
 ; APPLICANT: LUO, Peizhi
 ; TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES FOR DRUG DISCOVERY
 ; FILE REFERENCE: A-68126-1/RFT/RMS/RMK
 ; CURRENT FILING DATE: 2000-02-11
 ; PRIOR APPLICATION NUMBER: 60/120, 009
 ; PRIORITY FILING DATE: 1999-02-11
 ; PRIOR APPLICATION NUMBER: 60/131, 674
 ; PRIORITY FILING DATE: 1999-04-29
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 11
 ; LENGTH: 211
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
 ; US-09-502-984B-11

Query Match 82.6%; Score 1061; DB 5; Length 211;
 Best Local Similarity 94.3%; Pred. No. 2e-88; Mismatches 2; Indels 0; Gaps 0;
 Matches 199; Conservative 10; MisMatch 2; Indels 0; Gaps 0;

Query Match 82.9%; Score 1064; DB 5; Length 211;
 Best Local Similarity 94.3%; Pred. No. 1.1e-88; Mismatches 2; Indels 0; Gaps 0;
 Matches 199; Conservative 10; MisMatch 2; Indels 0; Gaps 0;

Qy 1 KFESKAALLAARGPPELCTERLUDLVCFFEEAASAGVPGNFNSFSQOLEDEPKWLCRL 60
 Db 1 KFESKAALLAARGPPELCTERLUDLVCFFEEAASAGVPGNFNSFSQOLEDEPKWLCRL 60

Qy 61 HQAPTAGVRFWCSLPTADTSFVPLRVTASGAPRHVTHINNEVLLDAPVGLV 120
 Db 61 HQAPTAGVRFWCSLPTADTSFVPLRVTASGAPRHVTHINNEVLLDAPVGLV 120

Qy 121 RLADSGHVVIRWLPPETPTMHSIRFIELDISAGNGAGSVORVELLEGRTCEVLNSLRGR 180
 Db 121 RLADSGHVVIRWLPPETPTMHSIRFIELDISAGNGAGSVORVELLEGRTCEVLNSLRGR 180

Qy 181 TRITAVRVARMAEPSFGGFWSAWSEPVSLT 211
 Db 181 TRITAVRVARMAEPSFGGFWSAWSEPVSLT 211

RESULT 14
 US-09-502-984B-2
 ; Sequence 2, Application US/09502984B
 ; GENERAL INFORMATION:
 ; APPLICANT: DUO, Peizhi
 ; TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES FOR DRUG DISCOVERY
 ; FILE REFERENCE: A-68126-1/RFT/RMS/RMK
 ; CURRENT FILING DATE: 2000-02-11
 ; PRIOR APPLICATION NUMBER: 60/120, 009
 ; PRIORITY FILING DATE: 1999-02-11
 ; PRIOR APPLICATION NUMBER: 60/131, 674
 ; PRIORITY FILING DATE: 1999-04-29
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 211
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-502-984B-2

Query Match 82.6%; Score 1060; DB 5; Length 211;
 Best Local Similarity 93.8%; Pred. No. 2.5e-88; Mismatches 2; Indels 0; Gaps 0;
 Matches 198; Conservative 11; MisMatch 2; Indels 0; Gaps 0;

Qy 1 KFESKAALLAARGPPELCTERLUDLVCFFEEAASAGVPGNFNSFSQOLEDEPKWLCRL 60
 Db 1 KFESKAALLAARGPPELCTERLUDLVCFFEEAASAGVPGNFNSFSQOLEDEPKWLCRL 60

Qy 61 HQAPTAGVRFWCSLPTADTSFVPLRVTASGAPRHVTHINNEVLLDAPVGLV 120
 Db 61 HQAPTAGVRFWCSLPTADTSFVPLRVTASGAPRHVTHINNEVLLDAPVGLV 120

Qy 121 RLADSGHVVIRWLPPETPTMHSIRFIELDISAGNGAGSVORVELLEGRTCEVLNSLRGR 180
 Db 121 RLADSGHVVIRWLPPETPTMHSIRFIELDISAGNGAGSVORVELLEGRTCEVLNSLRGR 180

Qy 181 TRITAVRVARMAEPSFGGFWSAWSEPVSLT 211
 Db 181 TRITAVRVARMAEPSFGGFWSAWSEPVSLT 211

RESULT 15
 US-09-502-984B-12
 ; Sequence 12, Application US/09502984B
 ; GENERAL INFORMATION:
 ; APPLICANT: Luo, Peizhi
 ; TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES FOR DRUG DISCOVERY
 ; FILE REFERENCE: A-68126-1/RFT/RMS/RMK
 ; CURRENT APPLICATION NUMBER: US/09/502, 984B
 ; CURRENT FILING DATE: 2000-02-11
 ; PRIOR APPLICATION NUMBER: 60/120, 009
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 ; PRIOR APPLICATION NUMBER: 60/131, 674
 ; PRIORITY FILING DATE: 1999-04-29
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 12

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; Sequence 10, Application US/09502994B
; GENERAL INFORMATION:
; APPLICANT: Luo, Peizhi
; TITLE OF INVENTION: STRUCTURE-BASED SCREENING TECHNIQUES FOR DRUG DISCOVERY
; FILE REFERENCE: A-68126-1/RFT/RMS/RMK
; CURRENT APPLICATION NUMBER: US/09/502,984B
; CURRENT FILING DATE: 2000-02-11
; PRIORITY APPLICATION NUMBER: 60/120, 009
; PRIORITY FILING DATE: 1999-02-11
; PRIORITY FILING DATE: 1999-04-29
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
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; LENGTH: 211
; TYPE: PRN
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; US-09-502-984B-10

Query Match 82.6%; Score 1060; DB 5; Length 211;
Best Local Similarity 93.8%; Pred. No. 2.5e-88; 2; Indels 0; Gaps 0;
Matches 198; Conservative 11; Mismatches 2;

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Db	1	KFESKAALLAARGPPEELCFTERLEDIVCFWBEABASAGVGPGNFSTSFOLEDEPWKLICRL	60
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Db	61	HQAPPTARGAVRFWCSLPHADISSFVPLRVLVIAASGAPRYHRVTHNEWVLLDAPVGLVA	120
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Db	121	RLADESQHVWVRLPPETPMSSHIRELDISAGNGAGSVQVLELEGRTCEVLSNURGR	180
QY	181	TRTTIAVRARMAPSPSGGFWSAWSEPVSLLT	211
Db	181	TRTTIAVRARMAPSPSGGFWSAWSEPVSLLT	211

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